

In the claims:

Please amend claims as follows:

-- 1. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (5):~~

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of the ~~sequence pairs~~ SEQ ID NOS: (69) and (74), SEQ ID NOS: (69) and (78), SEQ IDS NOS: (72) and (71), SEQ ID NOS: (72) and (74), and SEQ ID NOS: (72) and (78);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) isolating said DNA fragment;

(4) determining the nucleotide sequence of said DNA fragment; and

(5) ~~identifying the microorganism by~~ comparing the sequence of the amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

2. (Currently Amended) The method for identifying a microorganism according to claim 1, wherein the amino acid sequence pairs that are used are ~~sequence pairs~~ SEQ ID NOS: (69) and (74), SEQ ID NOS: (69) and (78), SEQ ID NOS: (72) and (74), or SEQ ID NOS: (72) and (78); and said microorganism belongs to *proteobacteria*.

3. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (8):~~

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (69) and (71);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~

~~sequences~~ SEQ ID NOS: (70) and (71);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

4. (Currently Amended) A method for identifying a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of ~~amino-acid~~ sequences SEQ ID NOS: (69) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino-acid~~ sequences SEQ ID NOS: (69) and (73);

(4) synthesizing forward and reverse primers based on a single pair of ~~amino-acid~~ sequences SEQ ID NOS: (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

5. (Currently Amended) A method for identifying a microorganism, comprising the following steps (1) to (8):

(1) synthesizing forward and reverse primers based on a single pair of ~~amino-acid~~ sequences SEQ ID NOS: (72) and (74);

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to

produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~  
~~sequences~~ SEQ ID NOS: (72) and (73);

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~  
~~sequences~~ SEQ ID NOS: (70) and (74);

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of  
primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene  
DNA fragments to known *gyrB* gene DNA fragment sequences.

6. (Currently Amended) A method for identifying a microorganism, comprising ~~the~~  
~~following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~  
~~sequences~~ SEQ ID NOS: (72) and (73);

(2) synthesizing forward and reverse primers based on a single pair of amino acid  
sequences selected from the group consisting of SEQ ID NOS: (76) and (71), SEQ ID NOS: (76)  
and (74), or SEQ ID NOS: (76) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers  
to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene  
DNA fragments to known *gyrB* gene DNA fragment sequences.

7. (Currently Amended) A method for identifying a microorganism, comprising ~~the~~  
~~following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~  
~~sequences~~ SEQ ID NOS: (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: (79) and (71), SEQ ID NOS: (79) and (74), or SEQ ID NOS: (79) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

8. (Currently Amended) A method for identifying a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: (80) and (71), SEQ ID NOS (80) and (74), or SEQ ID NOS: (80) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

9. (Currently Amended) A method for detecting a microorganism, comprising the following steps (1) to (5):

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of ~~the sequence pairs~~ SEQ ID NOS: (69) and (74), SEQ ID NOS: (69) and (78), SEQ ID NOS: (72) and (71), SEQ ID NOS: (72) and (74), ~~and~~ SEQ ID NOS (72) and (78);

- (2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;
- (3) isolating said DNA fragment;
- (4) determining the nucleotide sequence of said DNA fragment; and
- (5) ~~detecting the microorganism by~~ comparing the nucleotide sequence of said amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

10. (Currently Amended) The method for detecting a microorganism according to claim 9, wherein the amino acid sequence pairs that are used are ~~sequence pairs~~ SEQ ID NOS: {69} and {74}, SEQ ID NOS: {69} and {78}, SEQ ID NOS: {72} and {74}, or SEQ ID NOS: {72} and {78}; and said microorganism belongs to *proteobacteria*.

11. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (8)~~:

- (1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: {69} and {71};
- (2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;
- (3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: {69} and {73};
- (4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: {70} and {71};
- (5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two primers to produce two *gyrB* gene DNA fragments;
- (6) isolating said two DNA fragments;
- (7) determining the nucleotide sequences of said two DNA fragments; and
- (8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

12. (Currently Amended) A method for detecting a microorganism, comprising ~~the~~

~~following steps (1) to (8):~~

- (1) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (69) and (74);
- (2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;
- (3) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (69) and (73);
- (4) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (70) and (74);
- (5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;
- (6) isolating said two DNA fragments;
- (7) determining the nucleotide sequences of said two DNA fragments; and
- (8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

13. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (8):~~

- (1) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (72) and (74);
- (2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;
- (3) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (72) and (73);
- (4) synthesizing forward and reverse primers based on a single pair of ~~amino-acid sequences~~ SEQ ID NOS: (70) and (74);
- (5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;
- (6) isolating said two DNA fragments;
- (7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

14. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6):~~

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (72) and (73);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: (76) and (71), SEQ ID NOS: (76) and (74), or SEQ ID NOS: (76) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

15. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6):~~

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: (79) and (71), SEQ ID NOS: (79) and (74), or SEQ ID NOS: (79) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

16. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6):~~

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: (69) and (77);

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: (80) and (71), SEQ ID NOS: (80) and (74), or SEQ ID NOS: (80) and (75);

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences. --